

FIG. 1

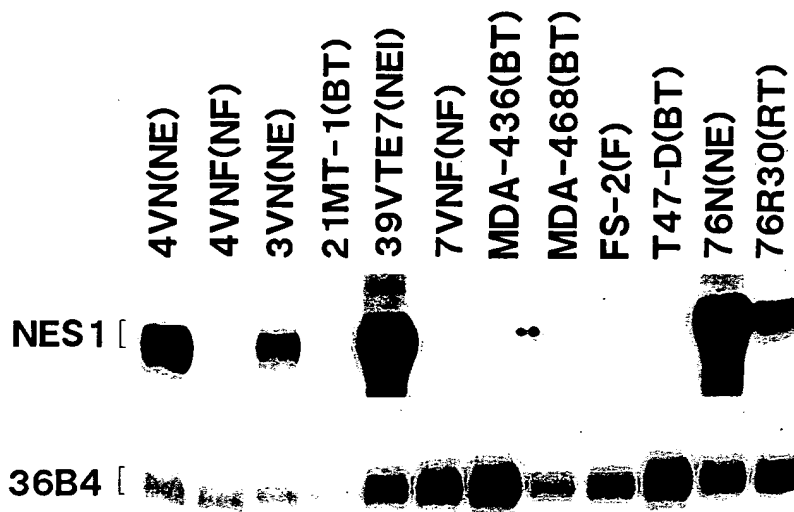


FIG. 2B

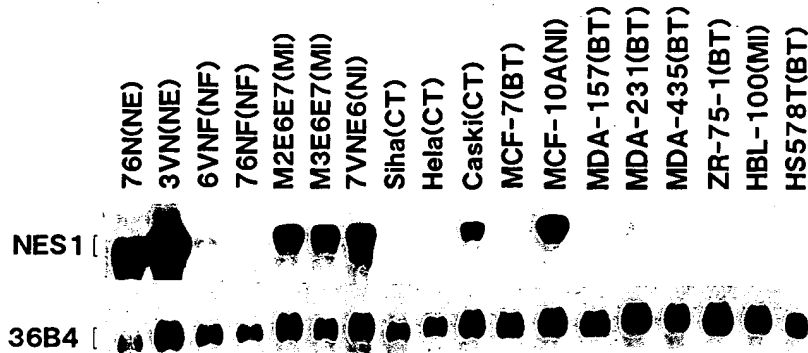


FIG. 2A

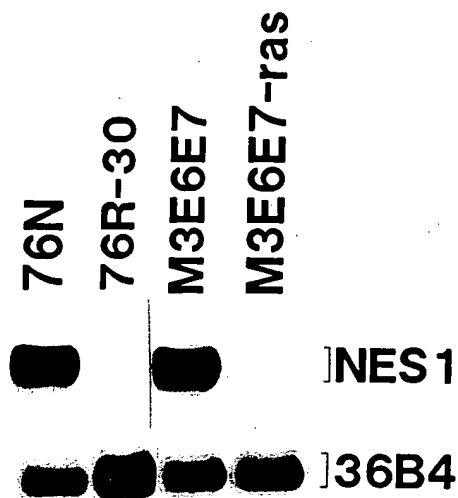


FIG. 3

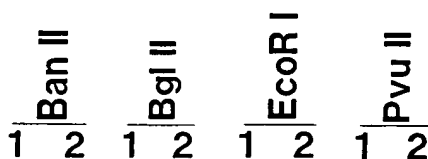


FIG. 4

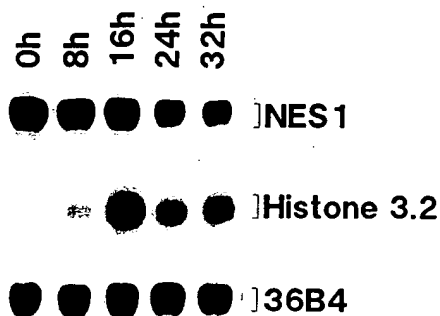


FIG. 5A

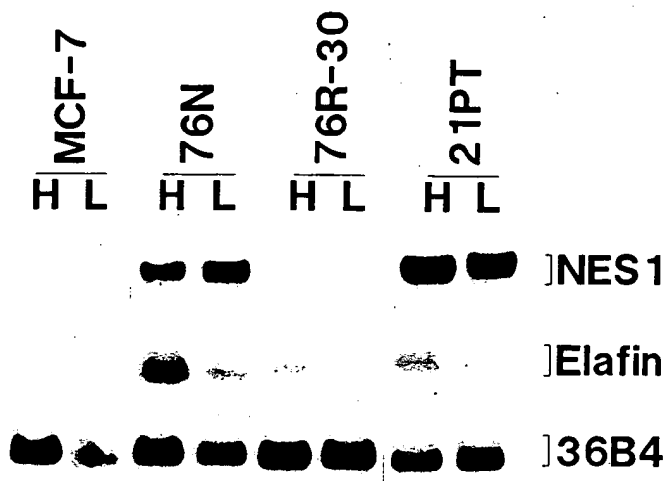


FIG. 6

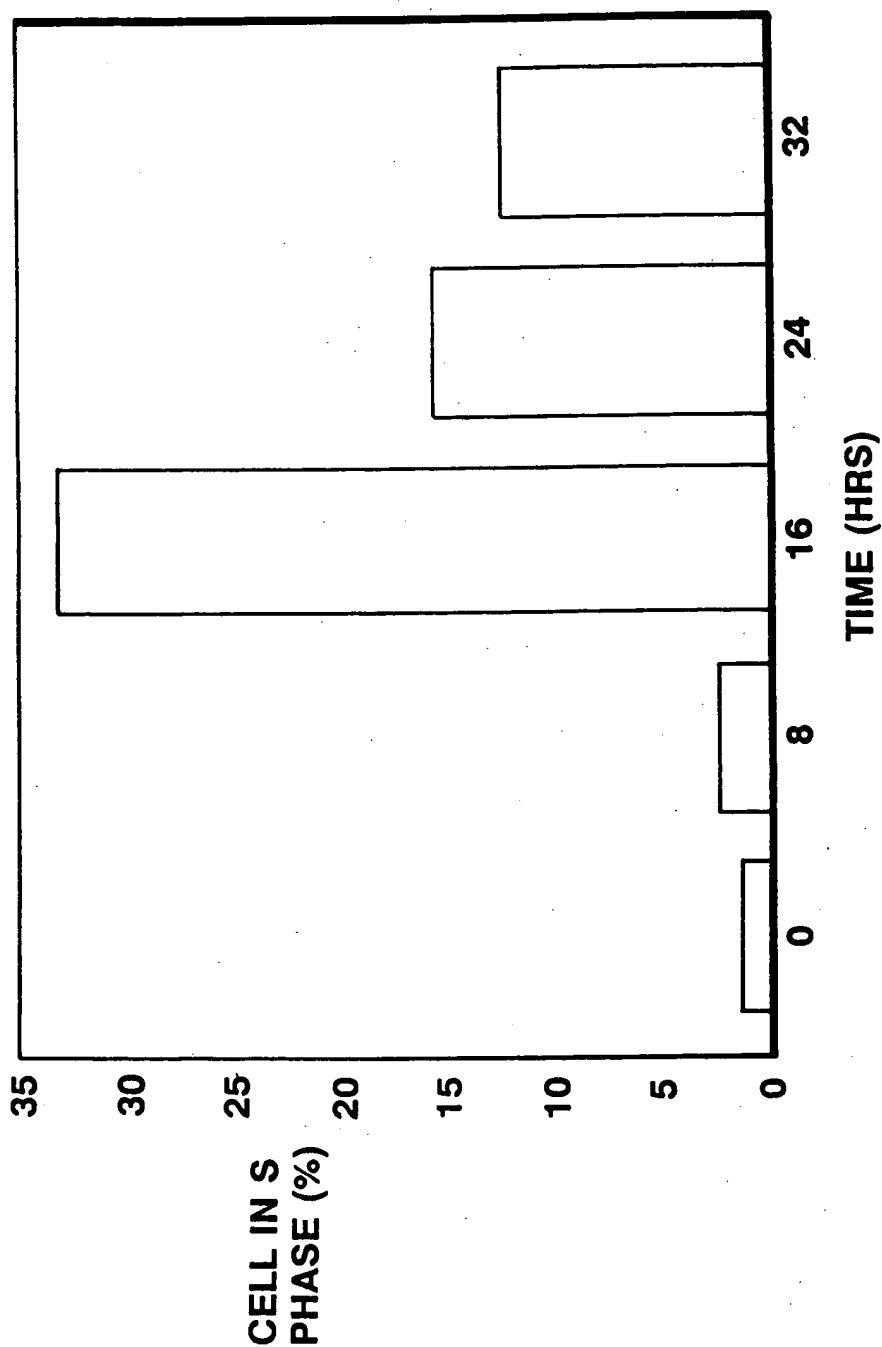


FIG. 5B

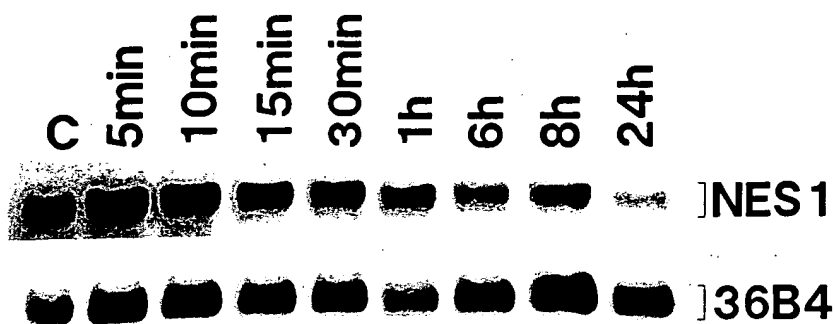


FIG. 7A

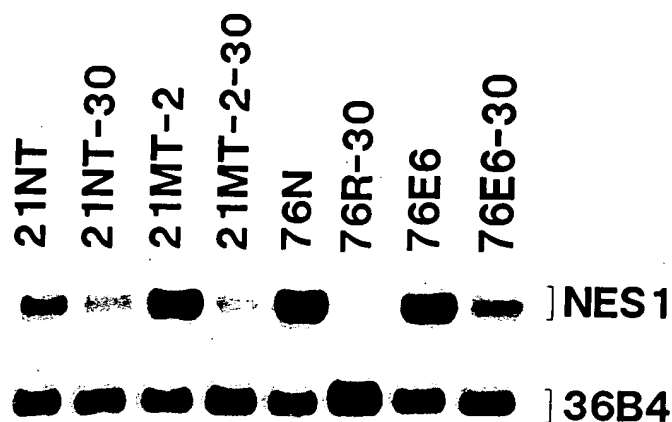


FIG. 7B

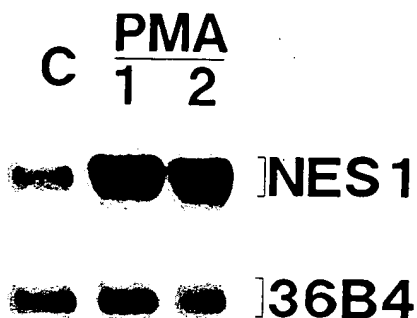


FIG. 8



Comparison of Sequences near putative active site

	86	137	223	224	227	228	229	230	231	241	243	245
NES 1	H	D	D	P	S	D	S	G	G	G	L	W
Human Pancreatic Trypsinogen III	H	D	D	S	R	D	S	G	G	G	V	W
	▲	▲	△	△			▲			△	△	△

▲: Catalytic triad

△: Residues important for substrate binding and specificity

FIG. 9A

Alignment of NES 1 amino acid sequence with other serine proteases

	1				50
Mmtryar	..MSALLILA	LVGA.....	AVAFFVDD.D	DKIVG...GY
HstryivbLELHP	LLGGRTWRAA	RDADGCEALG	TVAVPFDD.D	DKIVG...GY
Rntrypvb	..MKICIFFT	LLGT.....	VAAFPTEEND	DRIVG...GY
SstrypiiAAFATE..D	DKIVG...GY
Nes1	MRAPHLHLSA	ASGARALAKL	LPLLMAQLWA	AEAALLPQND	TRLDPEAYGA
	51				100
Mmtryar	TCRESSVPYQ	VSLNAGYHF.	CGGSLINDQW	VVSAAHCYKY	RIQVRLGEHN
Hstryivb	TC.ENS LPYQ	VSLNSGSHF.	CGGSLISEQW	VVSAAHCYKT	RIQVRLGEHN
Rntrypvb	TCQEHSPYQ	VSLNAGSHI.	CGGSLITDQW	VLSAAHCYHP	QLQVRLGEHN
Sstrypii	ECKAYSQPHQ	VSLNSGYHF.	CGGSLVNENW	VVSAAHCYQS	RVEVRLGEHN
Nes1	PCARGSQPWQ	VSLFNGLSFH	CAGVLVDQSW	VLTAAHCGNK	PLWARVGDH
	101				150
Mmtryar	INVLEGNEQF	VDSAKIIRHP	NYN.....	.SWTLDNDIM	LIKLASPVTL
Hstryivb	IKVLEGNEQF	INAAKIIRHP	KYN.....	.RDTLDNDIM	LICKSSPAVI
Rntrypvb	IYEIEGAEQF	IDAAMILHP	DYD.....	.KWTVDNDIM	LICKSKPATL
Sstrypii	IQVTEGSEQF	ISSSRVIRHP	NYS.....	.SYNIDNDIM	LICKSKPATL
Nes1	LLLQGEQL	RRTTRSVVHP	KYHQSGGPIL	PRRTDEHDL	LLKLARPVVP
	151		EXTRA INSERT		200
Mmtryar	NARVASVPLP	SSCAPAGTQC	LISGWGNTLS	NGVNNPDLLQ	CVDAPVLPQA
Hstryivb	NARVSTISLP	TAPPAAGTEC	LISGWGNTLS	FGADYPDELK	CLDAPVLTQA
Rntrypvb	NSKVSTIPLP	QYCPTAGTEC	LVSGWG.VLK	FGFESPSVLQ	CLDAPVLSDS
Sstrypii	NTYVQPVLP	TSCAPAGTMC	TVSGWGNTMS	STAD.KNKLQ	CLNIPILSYS
Nes1	GPRVRALQLP	YRCAQPGDQC	QVAGWGTAA	RRVKYNKGLT	CSSITILSPK
	201				250
Mmtryar	DCEASYPGDI	TNNMICVGFL	EGGKDSCQGD	SGGPVVCNGE	LQGVVSWG.Y
Hstryivb	ECKASYPGKI	TNSMFCVGFL	EGGKDSCQRD	SGGPVVCNGQ	LQGVVSWG.H
Rntrypvb	VCHKAYPRQI	TNNMFCLGFL	EGGKDSCQYD	SGGPVVCNGE	VQGVVSWG.D
Sstrypii	DCNNSYPGMI	TNAMFCAGYL	EGGKDSCQGD	SGGPVVCNGE	LQGVVSWG.Y
Nes1	ECEVFYPGVV	TNNMICAG.L	DRGQDPCQSD	SGGPLVCDET	LQGLVSWGVY
	251		280		
Mmtryar	GCAQPDAPGV	YTKVCNYVDW	IQNTIADN*.		
Hstryivb	GCAWKNRPGV	YTKVINYVDW	IKDTIAANS*		
Rntrypvb	GCALEGKPGV	YTKVCNYLNV	IQQTVAAN*.		
Sstrypii	GCAEPGNPGV	YAKVCIFNDW	LTSTMATY*.		
Nes1	PCGSAQHPAV	YTQICKYMSW	INKVIRSN*.		

FIG. 9B



1 MRAPHLHLSA ASGARALAKL LPLLMAQLWA AEAALLPQND TRLDPEAYGA
51 PCARGSQPWQ VSLFNGLSFH CAGVLVDQSW VLTAAHCGNK PLWARVGDDH
101 LLLQGEQLR RTTRSVVHPK YHQSGPILP RRTDEHDLML LKLARPVVPG
151 PRVRALQLPY RCAQPGDQCQ VAGWGTTAAR RVKYNKGLTC SSITILSPKE
201 CEVFYPGVVT NNMICAGLDR GQDPCQSDSG GPLVCDETLQ GILSWGVPYC
251 GSAQHPAVYT QICKYMSWIN KVIRSN* (SEQ ID NO: 1)

FIG. 10



1 ACCAGCGGCA GACCACAGGC AGGGCAGAGG CACGTCTGGG TCCCCTCCCT
51 CCTTCCTATC GCGGACTCCC AGATCCTGGC CATGAGAGCT CCGCACCTCC
101 ACCTCTCCGC CGCCTCTGGC GCCCGGGCTC TGGCGAAGCT GCTGCCGCTG
151 CTGATGGCGC AACTCTGGGC CGCAGAGGCG GCGCTGCTCC CCCAAAACGA
201 CACGCGCTTG GACCCCGAAG CCTATGGCGC CCCGTGCGCG CGCGGCTCGC
251 AGCCCTGGCA GGTCTCGCTC TTCAACGGCC TCTCGTTCCA CTGCGCGGGT
301 GTCCTGGTGG ACCAGAGTTG GGTGCTGACG GCCGCGCACT GCGGAAACAA
351 GCCACTGTGG GCTCGAGTAG GGGATGATCA CCTGCTGCTT CTTCAGGGCG
401 AGCAGCTCCG CCGGACGACT CGCTCTGTTG TCCATCCCAA GTACCACCAG
451 GGCTCAGGCC CCATCCTGCC AAGGCGAACG GATGAGCACG ATCTCATGTT
501 GCTAAAGCTG GCCAGGCCCC TAGTGCCGGG GCCCCGCGTC CGGGCCCTGC
551 AGCTTCCCTA CCGCTGTGCT CAGCCCGGAG ACCAGTGCCA GGTGTGCTGGC
601 TGGGGCACCA CGGCCGCCCC GAGAGTGAAG TACAACAAGG GCCTGACCTG
651 CTCCAGCATC ACTATCCTGA GCCCTAAAGA GTGTGAGGTC TTCTACCCTG
701 GCGTGGTCAC CAACAACATG ATATGTGCTG GACTGGACCG GGGCCAGGAC
751 CCTTGCCAGA GTGACTCTGG AGGCCCCCTG GTCTGTGACG AGACCCTCCA
801 AGGCATCCTC TCGTGGGGTG TTTACCCCTG TGGCTCTGCC CAGCATCCAG
851 CTGTCTACAC CCAGATCTGC AAATACATGT CCTGGATCAA TAAAGTCATA
901 CGCTCCAACCT GATCCAGATG CTACGCTCCA GCTGATCCAG ATGTTATGCT
951 CCTGCTGATC CAGATGCCCC GAGGCTCCAT CGTCCATCCT CTTCCCTCCCC
1001 AGTCGGCTGA ACTCTCCCCT TGTCTGCACT GTTCAAACCT CTGCCGCCCT
1051 CCACACCTCT AAACATCTCC CCTCTCACCT CATTCCCCCA CCTATCCCCA
1101 TTCTCTGCCT GTACTGAAGC TGAAATGCAG GAAGTGGTGG CAAAGGTTTA
1151 TTCCAGAGAA GCCAGGAAGC CGGTCATCAC CCAGCCTCTG AGAGCAGTTA
1201 CTGGGGTCAC CCAACCTGAC TTCCTCTGCC ACTCCCCGCT GTGTGACTTT
1251 GGGCAAGCCA AGTGCCCTCT CTGAACCTCA GTTTCCTCAT CTGCAAAATG
1301 GGAACAATGA CGTGCCTACC TCTTAGACAT GTTGTGAGGA GACTATGATA
1351 TAACATGTGT ATGTAAATCT TCATGTGATT GTCATGTAAG GCTTAACACA
1401 GTGGGTGGTG AGTTCTGACT AAAGGTTACC TGTTGTCGTG AAAAAAAAAA
1451 AAAA (SEQ ID NO: 2)

FIG. 11